

OIEP

RAW SEQUENCE LISTING DATE: 08/18/2000
 PATENT APPLICATION: US/09/634,109 TIME: 14:19:15

Input Set : A:\6202NCPseq.txt
 Output Set: N:\CRF3\08182000\I634109.raw

4 <110> APPLICANT: Gabriel Vogeli
 5 Linda S. Wood
 7 <120> TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR EXPRESSED IN BRAIN
 9 <130> FILE REFERENCE: 28341/6202NCP
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/634,109
 C--> 12 <141> CURRENT FILING DATE: 2000-08-08
 14 <150> PRIOR APPLICATION NUMBER: US 09/377,563
 15 <151> PRIOR FILING DATE: 2000-08-19 1999-08-19
 17 <160> NUMBER OF SEQ ID NOS: 12
 19 <170> SOFTWARE: PatentIn Ver. 2.0
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 948
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Homo sapiens
 26 <220> FEATURE:
 27 <221> NAME/KEY: CDS,
 28 <222> LOCATION: (1)..(945)
 30 <400> SEQUENCE: 1
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 32 Met Gly Arg Trp Val Asn Gln Ser Tyr Thr Asp Gly Phe Phe Leu Leu
 33 1 5 10 15
 35 ggc atc ttt tcc cac agc cag act gac ctt gtc ctc ttc tct gca gtt 96
 36 Gly Ile Phe Ser His Ser Gln Thr Asp Leu Val Leu Phe Ser Ala Val
 37 20 25 30
 39 atg gtg gtc ttc aca gtg gcc ctc tgt ggg aat gtc ctc ctc atc ttc 144
 40 Met Val Val Phe Thr Val Ala Leu Cys Gly Asn Val Leu Leu Ile Phe
 41 35 40 45
 43 ctc atc tac ctg gac gct gga ctt cac acc ccc atg tac ttc ttc ctc 192
 44 Leu Ile Tyr Leu Asp Ala Gly Leu His Thr Pro Met Tyr Phe Phe Leu
 45 50 55 60
 47 agc cag ctc tcc ctc atg gac ctc atg ttg gtc tgt aac att gtg cca 240
 48 Ser Gln Leu Ser Leu Met Asp Leu Met Leu Val Cys Asn Ile Val Pro
 49 65 70 75 80
 51 aag atg gca gcc aac ttc ctg tct ggc agg aag tcc atc tcc ttt gtg 288
 52 Lys Met Ala Ala Asn Phe Leu Ser Gly Arg Lys Ser Ile Ser Phe Val
 53 85 90 95
 55 ggc tgt ggc ata caa att ggc ttt ttt gtc tct ctt gtg gga tct gag 336
 56 Gly Cys Gly Ile Gln Ile Gly Phe Phe Val Ser Leu Val Gly Ser Glu
 57 100 105 110
 59 ggg ctc ttg ctg gga ctc atg gct tat gac cac tac gtg gcc gtt agc 384
 60 Gly Leu Leu Leu Gly Leu Met Ala Tyr Asp His Tyr Val Ala Val Ser
 61 115 120 125
 64 cac cca ctt cac tat ccc atc ctc atg aat cag agg gtc tgt ctc cag 432
 65 His Pro Leu His Tyr Pro Ile Leu Met Asn Gln Arg Val Cys Leu Gln
 66 130 135 140
 68 att act ggg agc tcc tgg gcc ttt ggg ata ata gat gga gtg att cag 480
 69 Ile Thr Gly Ser Ser Trp Ala Phe Gly Ile Ile Asp Gly Val Ile Gln

Does Not Comply
 Corrected Diskette Needed

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70 145                      150                      155                      160
72 atg gtg gca gcc atg ggc tta cct tac tgt ggc tca agg agc gtg gat    528
73 Met Val Ala Ala Met Gly Leu Pro Tyr Cys Gly Ser Arg Ser Val Asp
74                      165                      170                      175
76 cac ttt ttc tgt gag gta caa gct tta ttg aag ctg gcc tgt gca gac    576
77 His Phe Phe Cys Glu Val Gln Ala Leu Leu Lys Leu Ala Cys Ala Asp
78                      180                      185                      190
80 act tcc ctt ttt gac acc ctc ctc ttt gct tgc tgt gtc ttc atg ctt    624
81 Thr Ser Leu Phe Asp Thr Leu Leu Phe Ala Cys Cys Val Phe Met Leu
82                      195                      200                      205
84 ctc ctt ccc ttc tcc atc atc atg gcc tcc tat gct tgc atc cta ggg    672
85 Leu Leu Pro Phe Ser Ile Ile Met Ala Ser Tyr Ala Cys Ile Leu Gly
86                      210                      215                      220
88 gct gtg ctc cga ata cgc tct gct cag gcc tgg aaa aaa gcc ctg gcc    720
89 Ala Val Leu Arg Ile Arg Ser Ala Gln Ala Trp Lys Lys Ala Leu Ala
90 225                      230                      235                      240
92 acc tgc tcc tcc cac cta aca gct gtc acc ctc ttc tat ggg gca gcc    768
93 Thr Cys Ser Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Ala Ala
94                      245                      250                      255
96 atg ttc atg tac ctg agg cct agg cgc tac cgg gcc cct agc cat gac    816
97 Met Phe Met Tyr Leu Arg Pro Arg Tyr Arg Ala Pro Ser His Asp
98                      260                      265                      270
100 aag gtg gcc tct atc ttc tac aca gtc ctt act ccc atg ctg aac ccc    864
101 Lys Val Ala Ser Ile Phe Tyr Thr Val Leu Thr Pro Met Leu Asn Pro
102                      275                      280                      285
104 ctc att tac agc ttg agg aat ggg gag gtg atg ggg gca ctg agg aag    912
105 Leu Ile Tyr Ser Leu Arg Asn Gly Glu Val Met Gly Ala Leu Arg Lys
106                      290                      295                      300
108 ggg ctg gac cgc tgc agg att ggc agc cag cac tga                      948
109 Gly Leu Asp Arg Cys Arg Ile Gly Ser Gln His
110 305                      310                      315
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115 <212> TYPE: PRT
116 <213> ORGANISM: Homo sapiens
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122 Gly Ile Phe Ser His Ser Gln Thr Asp Leu Val Leu Phe Ser Ala Val
123                      20                      25                      30
126 Met Val Val Phe Thr Val Ala Leu Cys Gly Asn Val Leu Leu Ile Phe
127                      35                      40                      45
129 Leu Ile Tyr Leu Asp Ala Gly Leu His Thr Pro Met Tyr Phe Phe Leu
130                      50                      55                      60
132 Ser Gln Leu Ser Leu Met Asp Leu Met Leu Val Cys Asn Ile Val Pro
133 65                      70                      75                      80
135 Lys Met Ala Ala Asn Phe Leu Ser Gly Arg Lys Ser Ile Ser Phe Val
136                      85                      90                      95
138 Gly Cys Gly Ile Gln Ile Gly Phe Phe Val Ser Leu Val Gly Ser Glu

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139          100          105          110
141 Gly Leu Leu Leu Gly Leu Met Ala Tyr Asp His Tyr Val Ala Val Ser
142          115          120          125
144 His Pro Leu His Tyr Pro Ile Leu Met Asn Gln Arg Val Cys Leu Gln
145          130          135          140
147 Ile Thr Gly Ser Ser Trp Ala Phe Gly Ile Ile Asp Gly Val Ile Gln
148 145          150          155          160
150 Met Val Ala Ala Met Gly Leu Pro Tyr Cys Gly Ser Arg Ser Val Asp
151          165          170          175
153 His Phe Phe Cys Glu Val Gln Ala Leu Leu Lys Leu Ala Cys Ala Asp
154          180          185          190
156 Thr Ser Leu Phe Asp Thr Leu Leu Phe Ala Cys Cys Val Phe Met Leu
157          195          200          205
159 Leu Leu Pro Phe Ser Ile Ile Met Ala Ser Tyr Ala Cys Ile Leu Gly
160          210          215          220
162 Ala Val Leu Arg Ile Arg Ser Ala Gln Ala Trp Lys Lys Ala Leu Ala
163 225          230          235          240
165 Thr Cys Ser Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Ala Ala
166          245          250          255
168 Met Phe Met Tyr Leu Arg Pro Arg Arg Tyr Arg Ala Pro Ser His Asp
169          260          265          270
171 Lys Val Ala Ser Ile Phe Tyr Thr Val Leu Thr Pro Met Leu Asn Pro
172          275          280          285
174 Leu Ile Tyr Ser Leu Arg Asn Gly Glu Val Met Gly Ala Leu Arg Lys
175          290          295          300
177 Gly Leu Asp Arg Cys Arg Ile Gly Ser Gln His
178 305          310          315
181 <210> SEQ ID NO: 3
182 <211> LENGTH: 22
183 <212> TYPE: DNA
184 <213> ORGANISM: Artificial Sequence
186 <220> FEATURE:
187 <223> OTHER INFORMATION: Description of Artificial Sequence: PRIMER
188 SEQUENCE
190 <400> SEQUENCE: 3
191 gcctctatct tctacacagt cc 22
194 <210> SEQ ID NO: 4
195 <211> LENGTH: 20
196 <212> TYPE: DNA
197 <213> ORGANISM: Artificial Sequence
199 <220> FEATURE:
200 <223> OTHER INFORMATION: Description of Artificial Sequence: PRIMER
201 SEQUENCE
203 <400> SEQUENCE: 4
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207 <210> SEQ ID NO: 5
208 <211> LENGTH: 59
209 <212> TYPE: DNA
210 <213> ORGANISM: Artificial Sequence

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212 <220> FEATURE:
213 <223> OTHER INFORMATION: Description of Artificial Sequence: PRIMER
214 SEQUENCE
216 <400> SEQUENCE: 5
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221 <211> LENGTH: 60
222 <212> TYPE: DNA
223 <213> ORGANISM: Artificial Sequence.
225 <220> FEATURE:
226 <223> OTHER INFORMATION: Description of Artificial Sequence: PRIMER
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229 <400> SEQUENCE: 6
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234 <211> LENGTH: 9
235 <212> TYPE: PRT
236 <213> ORGANISM: Artificial Sequence
238 <220> FEATURE:
239 <223> OTHER INFORMATION: Description of Artificial Sequence: MAP KINASE
240 SUBSTRATE PEPTIDE
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244 1 5
247 <210> SEQ ID NO: 8
248 <211> LENGTH: 316
249 <212> TYPE: PRT
250 <213> ORGANISM: Homo sapiens
252 <400> SEQUENCE: 8
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254 1 5 10 15
256 Glu His Pro Gly Leu Gly Arg Thr Leu Phe Val Asp Val Ile Thr Ser
257 20 25 30
259 Tyr Leu Leu Thr Leu Val Gly Asn Thr Leu Ile Ile Leu Leu Ser Ala
260 35 40 45
262 Leu Asp Thr Lys Leu His Ser Pro Met Tyr Phe Phe Leu Ser Asn Leu
263 50 55 60
265 Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Cys Val Pro Gln Met Leu
266 65 70 75 80
268 Ala Asn Leu Trp Gly Pro Lys Lys Thr Ile Ser Phe Leu Asp Cys Ser
269 85 90 95
271 Val Gln Ile Phe Ile Phe Leu Ser Leu Gly Thr Thr Glu Cys Ile Leu
272 100 105 110
274 Met Lys Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys Gln Pro Leu
275 115 120 125
277 His Tyr Ala Thr Ile Ile His Pro Arg Leu Cys Trp Gln Leu Ala Ser
278 130 135 140
281 Val Ala Trp Val Ile Gly Leu Val Gly Ser Val Val Gln Thr Pro Ser
282 145 150 155 160

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284 Thr Leu His Leu Pro Phe Cys Pro Asp Arg Gln Val Asp Asp Phe Val
285           165           170           175
287 Cys Glu Val Pro Ala Leu Ile Arg Leu Ser Cys Glu Asp Thr Ser Tyr
288           180           185           190
290 Asn Glu Ile Gln Val Ala Val Ala Ser Val Phe Ile Leu Val Val Pro
291           195           200           205
293 Leu Ser Leu Ile Leu Val Ser Tyr Gly Ala Ile Thr Trp Ala Val Leu
294           210           215           220
296 Arg Ile Asn Ser Ala Thr Ala Trp Arg Lys Ala Phe Gly Thr Cys Ser
297 225           230           235           240
299 Ser His Leu Thr Val Val Thr Leu Phe Tyr Ser Ser Val Ile Ala Val
300           245           250           255
302 Tyr Leu Gln Pro Lys Asn Pro Tyr Ala Gln Gly Arg Gly Lys Phe Phe
303           260           265           270
305 Gly Leu Phe Tyr Ala Val Gly Thr Pro Ser Leu Asn Pro Leu Val Tyr
306           275           280           285
308 Thr Leu Arg Asn Lys Glu Ile Lys Arg Ala Leu Arg Arg Leu Leu Gly
309           290           295           300
312 Lys Glu Arg Asp Ser Arg Glu Ser Trp Arg Ala Ala
313 305           310           315
316 <210> SEQ ID NO: 9
317 <211> LENGTH: 223
318 <212> TYPE: PRT
319 <213> ORGANISM: Mus musculus
321 <400> SEQUENCE: 9
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325 Lys Met Ala Val Asn Phe Leu Ser Gly Arg Lys Ser Ile Ser Phe Ala
326           20           25           30
328 Gly Cys Gly Ile Gln Ile Gly Phe Phe Val Ser Leu Val Gly Ser Glu
329           35           40           45
331 Gly Leu Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Ser
332           50           55           60
334 His Pro Leu His Tyr Pro Ile Leu Met Ser Gln Lys Val Cys Leu Gln
335   65           70           75           80
337 Ile Ala Gly Ser Ser Trp Ala Phe Gly Ile Leu Asp Gly Ile Ile Gln
338           85           90           95
340 Met Val Ala Ala Met Ser Leu Pro Tyr Cys Gly Ser Arg Tyr Ile Asp
341           100          105          110
343 His Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ala Cys Ala Asp
344           115          120          125
346 Thr Ser Leu Phe Asp Thr Leu Leu Phe Ala Cys Cys Val Phe Met Leu
347           130          135          140
349 Leu Leu Pro Phe Ser Ile Ile Val Thr Ser Tyr Ala Arg Ile Leu Gly
350 145           150          155          160
352 Ala Val Leu Arg Met His Ser Ala Gln Ser Arg Lys Lys Ala Leu Ala
353           165          170          175
355 Thr Cys Ser Ser His Leu Thr Ala Val Ser Leu Phe Tyr Gly Ala Ala
356           180          185          190

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VERIFICATION SUMMARY DATE: 08/18/2000
PATENT APPLICATION: US/09/634,109 TIME: 14:19:16

Input Set : A:\6202NCPseq.txt
Output Set: N:\CRF3\08182000\I634109.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date